RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/590,171_

Source: _1FWP_

Date Processed by STIC: _8/30/06_

ENTERED

IFWP

RAW SEQUENCE LISTING   DATE: 08/30/2006
PATENT APPLICATION: US/10/590,171   TIME: 09:06:53

Input Set : A:\P03371US0 Sequence listing).txt
Output Set: N:\CRF4\08302006\J590171.raw

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   5 <120> TITLE OF INVENTION: 2031 OXIDOREDUCTASE
   7 <130> FILE REFERENCE: HO-P03371US0
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/590,171
C--> 10 <141> CURRENT FILING DATE: 2006-08-18
  12 <150> PRIOR APPLICATION NUMBER: GB 0403746.1
  13 <151> PRIOR FILING DATE: 2004-02-19
  15 <150> PRIOR APPLICATION NUMBER: GB 0424080.0
  16 <151> PRIOR FILING DATE: 2004-10-29
  18 <160> NUMBER OF SEQ ID NOS: 101
  20 <170> SOFTWARE: PatentIn version 3.2
  22 <210> SEQ ID NO: 1
  23 <211> LENGTH: 1908
  24 <212> TYPE: DNA
  25 <213> ORGANISM: Aspergillus fumigatus
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  32 ctgtctccac tattcggcaa gattgtaaat caagcctgaa gaagcggagc aattcttgga     180
  34 agtcgtatgt tctactgatt tctgtgcctg gcgcagacgg gtatataaat aaagatcacc     240
  36 gcaccgagga gtttcttacc aacccatcaa taaccatcca caatctccta caacaaaat      300
  38 gactgtcgcc gatatcgacg ttcctcctgc cgagggcatc ccctacttca ctccggccca     360
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  68 tggaagtcgg aggataccgt gcggttcgcg caggagctgg tcaagcaggg cgccgttgat    1260
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  74 gccgtgggtg ccatcaccaa cggcaagcag gcgaatcaga ttctagagga gcaggatatc    1440
  76 gacgttgcgc tggttggccg tgggttccag aaggatcccg gtctggcctg acgtttgct     1500
  78 cagcacctcg gcgtcgaaat ctccatggcc aaccagatcc gctggggctt cacccggcgt    1560
  80 ggaggcaccc cgtacattga tccttcggtg tacaagcagt ctattttcga tgtatagagt    1620
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Output Set: **N:\CRF4\08302006\J590171.raw**

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 86 ttcgttctat tctactccaa tcgcaacgca tggcgaccac ggatcgagtc gaatttctcc   1800
 88 gtcgttcgta tctgatcaat ataaaaagcg gggaatggct tgaccccgcg cagaatgtcg   1860
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 94 <211> LENGTH: 1445
 95 <212> TYPE: DNA
 96 <213> ORGANISM: Aspergillus fumigatus
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103 gtcgccgata tcgacgttcc tcctgccgag ggcatcccct acttcactcc ggcccagaac   180
105 cctcctgccg gtacggcagc taaccccag accaatggcc agaagatccc caagctcttc   240
107 acgcccttga ccatccgtgg cgtcaccttc cagaaccgcc ttggtctcgc gcccctctgc   300
109 caatactccg cccaggacgg ccacatgacc gactaccaca tcgcccatct gggtgggatc   360
111 gcccaacgcg gacccggcct gatgctgatt gaggcgaccg ccgtccagcc cgaaggccgc   420
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119 ggatggccgg acccgcgtca aagggcccgg cgatatcccc tttgcggagc ccttcgccaa   660
121 gcccaaggcc atgacgctgg atgagatcga gcagttcaag aaggactggg tggcggccac   720
123 gaagcgcgcc atcgccgccg gtgcggactt tgtcgagatt cacaatgcgc atggatacct   780
125 gctgtcgtca ttcctctcgc cggccgccaa caaccgcacg gaccagtacg gcgggtcgtt   840
127 cgagaaccgc atccggctgt ctctcgagat tgcgcagttg actcgggacg ccgtcggccc   900
129 tcatgtgccc gtttttcctgc gcatttcggc ctcggactgg tgcgaggaga ccctgccgga   960
131 gcagagctgg aagtcggagg ataccgtgcg gttcgcgcag gagctggtca agcagggcgc  1020
133 cgttgatctg atcgatatca gcagcggtgg tgttctcgcg cagcagaaga tcaagtccgg  1080
135 ccctgccttc caggtgcctt ttgccgtggc cgtgaagaag gccgtcggcg acaagctgct  1140
137 ggttgccgcc gtgggtgcca tcaccaacgg caagcaggcg aatcagattc tagaggagca  1200
139 ggatatcgac gttgcgctgg ttggccgtgg gttccagaag atcccggtc tggcctggac  1260
141 gtttgctcag cacctcggcg tcgaaatctc catggccaac cagatccgct ggggcttcac  1320
143 ccggcgtgga ggcaccccgt acattgatcc ttcggtgtac aagcagtcta ttttcgatgt  1380
145 atagagtata gatagagttg aagatgatac ctcatagacg atcaatggac ccttgcatat  1440
147 tattt                                                            1445
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151 <211> LENGTH: 422
152 <212> TYPE: PRT
153 <213> ORGANISM: Aspergillus fumigatus
155 <400> SEQUENCE: 3
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161 Phe Thr Pro Ala Gln Asn Pro Pro Ala Gly Thr Ala Ala Asn Pro Gln
162             20                  25                  30
165 Thr Asn Gly Gln Lys Ile Pro Lys Leu Phe Thr Pro Leu Thr Ile Arg
166         35                  40                  45
169 Gly Val Thr Phe Gln Asn Arg Leu Gly Leu Ala Pro Leu Cys Gln Tyr
170     50                  55                  60
173 Ser Ala Gln Asp Gly His Met Thr Asp Tyr His Ile Ala His Leu Gly
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174 65                    70               75                  80
177 Gly Ile Ala Gln Arg Gly Pro Gly Leu Met Leu Ile Glu Ala Thr Ala
178             85               90                  95
181 Val Gln Pro Glu Gly Arg Ile Thr Pro Gln Asp Val Gly Leu Trp Lys
182            100              105              110
185 Asp Ser Gln Ile Ala Pro Met Arg Arg Val Ile Asp Phe Val His Ser
186            115              120              125
189 Gln Gly Gln Lys Ile Gly Val Gln Leu Ala His Ala Gly Arg Lys Ala
190        130              135              140
193 Thr Thr Val Ala Pro Trp Ile Ser Phe Ser Ala Ile Ala Thr Glu Lys
194 145              150              155              160
197 Val Gly Gly Trp Pro Asp Arg Val Lys Gly Pro Gly Asp Ile Pro Phe
198            165              170              175
201 Ala Glu Pro Phe Ala Lys Pro Lys Ala Met Thr Leu Asp Glu Ile Glu
202            180              185              190
205 Gln Phe Lys Lys Asp Trp Val Ala Ala Thr Lys Arg Ala Ile Ala Ala
206            195              200              205
209 Gly Ala Asp Phe Val Glu Ile His Asn Ala His Gly Tyr Leu Leu Ser
210        210              215              220
213 Ser Phe Leu Ser Pro Ala Ala Asn Asn Arg Thr Asp Gln Tyr Gly Gly
214 225              230              235              240
217 Ser Phe Glu Asn Arg Ile Arg Leu Ser Leu Glu Ile Ala Gln Leu Thr
218            245              250              255
221 Arg Asp Ala Val Gly Pro His Val Pro Val Phe Leu Arg Ile Ser Ala
222            260              265              270
225 Ser Asp Trp Cys Glu Glu Thr Leu Pro Glu Gln Ser Trp Lys Ser Glu
226        275              280              285
229 Asp Thr Val Arg Phe Ala Gln Glu Leu Val Lys Gln Gly Ala Val Asp
230        290              295              300
233 Leu Ile Asp Ile Ser Ser Gly Gly Val Leu Ala Gln Gln Lys Ile Lys
234 305              310              315              320
237 Ser Gly Pro Ala Phe Gln Val Pro Phe Ala Val Ala Val Lys Lys Ala
238            325              330              335
241 Val Gly Asp Lys Leu Leu Val Ala Ala Val Gly Ala Ile Thr Asn Gly
242        340              345              350
245 Lys Gln Ala Asn Gln Ile Leu Glu Glu Gln Asp Ile Asp Val Ala Leu
246        355              360              365
249 Val Gly Arg Gly Phe Gln Lys Asp Pro Gly Leu Ala Trp Thr Phe Ala
250        370              375              380
253 Gln His Leu Gly Val Glu Ile Ser Met Ala Asn Gln Ile Arg Trp Gly
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257 Phe Thr Arg Arg Gly Gly Thr Pro Tyr Ile Asp Pro Ser Val Tyr Lys
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262            420
265 <210> SEQ ID NO: 4
266 <211> LENGTH: 1352
267 <212> TYPE: DNA
268 <213> ORGANISM: Aspergillus fumigatus
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275 cctcccaagc tcttccggcc gctttcggtg cggggtctga cctttcacaa tcgcattggc    180
277 gtgagtgcag tccaggcaat tatgctatcc atcctatgcg agcccttgca ttggaacagc    240
279 cgcttacagg gaatgataat gagtagctat cgccactctg ccaatactca gccgacgatg    300
281 gacacatgac tccctggcat atggcacatc ttggagggat tgcccagcga gggccaggat    360
283 tcttgatggt cgaggcaaca gcagtcgaac cggaaggcag gatcaccccg caggacctgg    420
285 gactatggaa agactcgcag attgagccat tgagccgcgt gatcgagttt gtccacagtc    480
287 agaaccagct tatcggcgtg cagatcgcac acgcaggtcg caaggccagc accgtcgcgc    540
289 catggctctc ggccaacgat accgcctccg agaagatggg cggctggcca ggccgcgtca    600
291 aaggcccgac aaatgtgccc ttcaccgtta agaaccctgt gccgaaggag atgaccaagc    660
293 aggatatcga ggatctgaag accgcctggg tggccgctgt caaacgggct gttaaggccg    720
295 gagccgactt tatcgagatc cacaatgcgc atggctatct tctgatgtcg ttcctctccc    780
297 ctgcggtcaa cacgagaaca gacgagtacg gaggcagttt tgagaatcgc atccggctca    840
299 gtctggagat cgccaagctc acccgcgaaa atgtgcccaa ggatatgcct gtcttcctgc    900
301 gggtctccgc caccgattgg ctggaggagg tgcagccgaa caagcccagc tggcgaggcg    960
303 tggacactgt ccgatttgcg aagatcctgg cagaaacggg ttacgttgac gtgcttgacg   1020
305 tgagcagtgg cggcactcat tcggagcagc atatccacgc gaagccaggc ttccaggcac   1080
307 cctttgctat tgccgtcaag aacgccgtcg gggacaaact cgcagtggca tcagtgggta   1140
309 tgattgccag cgcgcatttg gccaattcct tgttggagaa ggacggactg gaccttgtgc   1200
311 tggttggacg tggcttccag aagaacccgg ggctggtgtg ggcgtgggcc gacgagctga   1260
313 atgtagagat ctccatggct aatcagatcc gatggggttt ctcgcggcgc ggtgctggtc   1320
315 cttacctcag gaagaaactc gagaagatat aa                                 1352
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319 <211> LENGTH: 1266
320 <212> TYPE: DNA
321 <213> ORGANISM: Aspergillus fumigatus
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328 cctcccaagc tcttccggcc gctttcggtg cggggtctga cctttcacaa tcgcattggc    180
330 ctatcgccac tctgccaata ctcagccgac gatggacaca tgactccctg gcatatggca    240
332 catcttggag ggattgccca gcgagggcca ggattcttga tggtcgaggc aacagcagtc    300
334 gaaccggaag gcaggatcac cccgcaggac ctgggactat ggaaagactc gcagattgag    360
336 ccattgagcc gcgtgatcga gtttgtccac agtcagaacc agcttatcgg cgtgcagatc    420
338 gcacacgcag gtcgcaaggc cagcaccgtc gcgccatggc tctcggccaa cgataccgcc    480
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342 gttaagaacc ctgtgccgaa ggagatgacc aagcaggata tcgaggatct gaagaccgcc    600
344 tgggtggccg ctgtcaaacg ggctgttaag gccggagccg actttatcga gatccacaat    660
346 gcgcatggct atcttctgat gtcgttcctc tcccctgcgg tcaacacgag aacagacgag    720
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350 gaaaatgtgc ccaaggatat gcctgtcttc ctgcgggtct ccgccaccga ttggctggag    840
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354 ctggcagaaa cgggttacgt tgacgtgctt gacgtgagca gtggcggcac tcattcggag    960
356 cagcatatcc acgcgaagcc aggcttccag gcacccnttg ctattgccgt caagaacgcc   1020
358 gtcggggaca aactcgcagt ggcatcagtg ggtatgattg ccagcgcgca tttggccaat   1080
360 tccttgttgg agaaggacgg actggacctt gtgctggttg acgtggcttc cagaagaac   1140
362 ccggggctgg tgtgggcgtg gccgacgag ctgaatgtag agatctccat ggctaatcag   1200
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372 <213> ORGANISM: Aspergillus fumigatus
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380 Ile Ser Tyr Phe Thr Pro Ala Gln Glu Pro Pro Ala Gly Thr Ala Ala
381             20                  25                  30
384 Asn Pro Gln Ser Asp Gly Ser Ala Pro Pro Lys Leu Phe Arg Pro Leu
385         35                  40                  45
388 Ser Val Arg Gly Leu Thr Phe His Asn Arg Ile Gly Leu Ser Pro Leu
389     50                  55                  60
392 Cys Gln Tyr Ser Ala Asp Asp Gly His Met Thr Pro Trp His Met Ala
393 65                  70                  75                  80
396 His Leu Gly Gly Ile Ala Gln Arg Gly Pro Gly Phe Leu Met Val Glu
397             85                  90                  95
400 Ala Thr Ala Val Glu Pro Glu Gly Arg Ile Thr Pro Gln Asp Leu Gly
401             100                 105                 110
404 Leu Trp Lys Asp Ser Gln Ile Glu Pro Leu Ser Arg Val Ile Glu Phe
405         115                 120                 125
408 Val His Ser Gln Asn Gln Leu Ile Gly Val Gln Ile Ala His Ala Gly
409     130                 135                 140
412 Arg Lys Ala Ser Thr Val Ala Pro Trp Leu Ser Ala Asn Asp Thr Ala
413 145                 150                 155                 160
416 Ser Glu Lys Met Gly Gly Trp Pro Gly Arg Val Lys Gly Pro Thr Asn
417             165                 170                 175
420 Val Pro Phe Thr Val Lys Asn Pro Val Pro Lys Glu Met Thr Lys Gln
421             180                 185                 190
424 Asp Ile Glu Asp Leu Lys Thr Ala Trp Val Ala Ala Val Lys Arg Ala
425         195                 200                 205
428 Val Lys Ala Gly Ala Asp Phe Ile Glu Ile His Asn Ala His Gly Tyr
429     210                 215                 220
432 Leu Leu Met Ser Phe Leu Ser Pro Ala Val Asn Thr Arg Thr Asp Glu
433 225                 230                 235                 240
436 Tyr Gly Gly Ser Phe Glu Asn Arg Ile Arg Leu Ser Leu Glu Ile Ala
437             245                 250                 255
440 Lys Leu Thr Arg Glu Asn Val Pro Lys Asp Met Pro Val Phe Leu Arg
441         260                 265                 270
444 Val Ser Ala Thr Asp Trp Leu Glu Glu Val Gln Pro Asn Lys Pro Ser
445         275                 280                 285
448 Trp Arg Gly Val Asp Thr Val Arg Phe Ala Lys Ile Leu Ala Glu Thr
449     290                 295                 300
452 Gly Tyr Val Asp Val Leu Asp Val Ser Ser Gly Gly Thr His Ser Glu
453 305                 310                 315                 320
456 Gln His Ile His Ala Lys Pro Gly Phe Gln Ala Pro Phe Ala Ile Ala
457             325                 330                 335
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<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:27; Xaa Pos. 187
Seq#:38; Xaa Pos. 22,37,196,200,216

VERIFICATION SUMMARY   DATE: 08/30/2006
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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:2037 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:176
L:2476 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:16
M:341 Repeated in SeqNo=38